



PT senescence-induced deoxyhypusine synthase and eIF-5s, useful for  
PT inhibiting senescence in a plant when introduced in reverse orientation  
PT into the genome of the plant -  
XX  
Claim 5; Fig 13; 135pp; English.

CC The present sequence is the coding sequence for tomato eukaryotic  
CC initiation factor 5A (eIF-5A). The eIF-5A coding sequence, when  
CC introduced into a plant cell in reverse orientation, inhibits expression  
CC of the endogenous eIF-5A gene. The present sequence is useful for  
CC altering age-related senescence and/or environmental stress-related  
CC senescence, for inhibiting seed aging and for increasing seed yield in a  
CC plant. In addition, the inhibition of senescence in a plant results in  
CC increased resistance of the plant to environmental stress-induced and/or  
CC pathogen-induced senescence, increased plant biomass, delayed fruit  
CC softening and spoilage.

**SQ** Sequence 780 BP; 253 A; 141 C; 171 G; 215 T; 0 other;

Query Match	Score	DB	Length
100.0%	780;	22;	780;
100.0%	780;	22;	780;

Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	aagaaatccctaaagagagaaagaggaacccctaaagagagaaagaaatctgcgaagaaagaaac	60
Db	1	aagaaatcctaaagagagaaagagatcctaaagagagagaaatctgcgaagaaagaaac	60
Qy	61	catctttgagtcataaagacgaatgcgtggtgcctcaaaaattcccaacagacgtcgaaac	120
Db	61	catctttgagtcataaagacgaatgcgtggtgcctcaaaaattcccaacagacgtcgaaac	120
Qy	121	atccgtaagaagatggtataatcgttatcaaaaagcgccctctgaaagatgtgttgaaagtctcc	180
Db	121	atccgtaagaagatggtataatcgttatcaaaaagcgccctctgaaagatgtgttgaaagtctcc	180
Qy	181	actctcaaaaactcggaanaacacgacgacatgcgtcaaaatgtgacctttgttgcaattgacatttc	240
Db	181	actctcaaaaactcggaanaacacgacgacatgcgtcaaaatgtgacctttgttgcaattgacatttc	240
Qy	241	aattggaagaagaactcggaagataatcgtctcgctccctccacaattgtgatgtgcacaatgtc	300
Db	241	aattggaagaagaactcggaagataatcgtctcgctccctccacaattgtgatgtgcacaatgtc	300
Qy	301	aacccgtacacgaactacaaacgtgatgatatactcgaagaagatggtttgtctcaactcttacc	360
Db	301	aacccgtacacgaactacaaacgtgatgatatactcgaagaagatggtttgtctcaactcttacc	360
Qy	361	gaaatgtggaanaacaaacaaagaatgtgacctcaaggtcttcccaacgataaataatctgtcgaagcag	420
Db	361	gaaatgtggaanaacaaacaaagaatgtgacctcaaggtcttcccaacgataaataatctgtcgaagcag	420
Qy	421	gttcaaaagatggtgttcccaagaaagaaagaaagatctgtgtgtgtctgtatagtcttcgcgaatggtgc	480
Db	421	gttcaaaagatggtgttcccaagaaagaaagaaagatctgtgtgtgtctgtatagtcttcgcgaatggtgc	480
Qy	481	gaaagacgaatattaagcgctgttaagaagatgtttgtgacccaagaatattaatgtgcacgagac	540
Db	481	gaaagacgaatattaagcgctgttaagaagatgtttgtgacccaagaatattaatgtgcacgagac	540
Qy	541	ataatcaactgccaagaagctttaagaacatataatcctaaatgtgtgtactcttgatacaact	600
Db	541	ataatcaactgccaagaagctttaagaacatataatcctaaatgtgtgtactcttgatacaact	600
Qy	601	agatttcaaaacgtcttcttttgcacgttccaanaaagaagaagaagaactcgttctatgg	660
Db	601	agatttcaaaacgtcttcttttgcacgttccaanaaagaagaagaagaactcgttctatgg	660
Qy	661	cttggagaagaagtgtgtgcttttaagctttttgacgaacaaagtgtgaactatgtaaaattctac	720
Db	661	cttggagaagaagtatctgtgcttttgaagctttcttgcgacgaacaaagtgtgaactatgtaaaattctac	720
Qy	721	tttttttttttttgggttaaaataactgcgtcgttttaagtgtttttgcaaaaaaataaaaaaaa	780

Db 721 ttttttttttggcraaatactgctcgctttaatgtttgcacaaaaaaaaaaaaaa 780

## RESULT 2

ID AAF32056 standard; cDNA; 812 BP.

AC AAF32056;

DT 10-APR-2001 (first entry)

DE Carnation eIF-5A coding sequence.

KW eIF-5A; eukaryotic initiation factor 5A; senescence inhibition;

OS Dianthus sp.

PN W0200102592-A2.

PD 11-JAN-2001.

PF 06-JUL-2000; 2000WO-US18364.

PR 06-JUL-1999; 99US-0348675.

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DR P-PSDB; AAB666878.

PT Tomato, Arabidops

PT into the genome of the plant -

PS Claim 5; Fig 14; 135pp; English.

CC The present sequence is the coding sequence for carnation eukaryotic  
CC initiation factor 5A (eIF-5A). The eIF-5A coding sequence, when  
CC introduced into a plant cell in reverse orientation, inhibits expression  
CC of the endogenous eIF-5A gene. The present sequence is useful for  
CC altering age-related senescence and/or environmental stress-related  
CC senescence, for inhibiting seed aging and for increasing seed yield in a  
CC plant. In addition, the inhibition of senescence in a plant results in  
CC increased resistance of the plant to environmental stress-induced and/or  
CC pathogen-induced senescence, increased plant biomass, delayed fruit  
CC softening and spoilage.

50 Sequence 812 BP; 234 A; 152 C; 192 G; 234 T; 0 other;

Query Match	39.78;	Score 309.6;	DB 22;	Length 812;
Best Local Similarity	76.58;	Pred. No. 2.1e-71;		
Matches 380;	Conservative	0;	Mismatches 117;	Indels 0;
			Gaps	0;

OY	29	ctgagaggaagacatgctcgagcgaagaacacccatttgatcaaaagcagatgctgtg	88
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Db 233 ccaaatgctacttctgttgcattgacatttccaacgcaagaagctggaagatattgtcc 292  
Qy 269 cgcctccccaattgtgtgtgccaacatgttaaccgtgacagctatacaagctatgtata 328  
Db 293 cctcaatccccaattgtgtgttccacatgtccaacggtgtcgaatacaagctctgtata 352  
Qy 329 tctctgaagatgtgttctgtcacttcttactgaagaagtgaacaacccaagatgactca 388  
Db 353 tcaactgaagatgtgttctgttactgtctgcgactgacagtggtgacacaagatgactcta 412  
Qy 389 ggcctccccaacatgaataatctgcctgaagcaggttaagaatgggttccaagagaagaag 448  
Db 413 agcttccctctcatgtagggcccttgtgaagcagatgaaggaggttgaaggcggggaag 472  
Qy 449 attctgtggtctgttactgtctgcgacatggcgcaagacgaattaacgcgttaagatg 508  
Db 473 actgtattctgtcgaagtcagtgctgtgcaatggtgagagaagacgaatctgtgcctgaaggag 532  
Qy 509 ttgtaccagaagattag 525  
Db 533 ttagtgtgtgcaagtag 549  
RESULT 3  
AAC39165  
ID AAC39165 standard; DNA; 768 bp.  
AC AAC39165;  
XX 17-OCT-2000 (first entry)  
DE Zea mays DNA fragment SMO ID NO: 23616.  
XX  
KW Hybridization assay; genetic mapping; gene expression control;  
KW Protein identification; signal transduction pathway; metabolic;  
KW pathway; promoter; termination sequence; corn; ss.  
XX  
OS Zea mays subsp. mays.  
XX  
PN BP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
PF  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130549.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
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PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
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PR 01-JUN-1999; 99US-0137222.  
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PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
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PR 06-JUL-1999; 99US-0142390.  
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PR 27-JUL-1999; 99US-0145918.

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PR 25-OCT-1999; 99US-0161406.

PR 26-OCT-1999; 99US-0161359.  
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PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 39.2%; Score 306; DB 21; Length 768;  
Best Local Similarity 77.2%; Pred. No. 2e-70;  
Matches 372; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 43 atgtcgagcgaagaaacaccattttgagtcgaaggcagatctgtgtcctcaaaacttc 102  
DB 141 atgtcgagagagagacaccagtttcgagtcacagccgacgcgcctcccaagacctac 200  
QY 103 ccacacgaagcttggaacatccgcgaagatgtgtacatcgtttcaaaagcgctccctgc 162  
DB 201 ccgcagcagccgcgcacatccgcgaagacggtctacatcgtttcaaaagcagctccctgc 260  
QY 163 aaggttgttgaggtctccacttcaaaaacttggaacacagacatgcttaatgtcaattt 222  
DB 261 aaggttgttgaggtctccacttcaaaaacttggaacacagatggtatggtatcccaagtcacttt 320  
QY 223 gtgacatgtacattttcaaatggaagaacttggaagatatactgtccgtccccaact 282  
DB 321 gtgtgcatgtacgttttcaacgtggaagaagcttgagatattgttctcttccccaac 380  
QY 283 tgtgatgtgcacacatgttaacogtacgcactatcagctgatatctctgaagaatgt 342  
DB 381 tgtgatgttcccccagttgtatcgcactgtgatatcagctgatatcactcgtgaagaatgtga 440  
QY 343 ttgtgtcactcttcaacgtggaagaactggaacacacagatatacctcagcgtccaccggt 402  
DB 441 ttgtgtgaccttcttgcacgtgacacgtgacacactaagatatacctcagcgtccaccggt 500  
QY 403 gaaaatctgtcgaagcaggttaagaatgtgttccaggaagaagaatcttgtgtgtct 462  
DB 501 gaagcctctggaagccacatcacatcagacgagatatagtatgataagacccctccctgcagc 560  
QY 463 gttatgtcgcgtgtggaagagcagataacgcgcgttaagagatgttgttacaagaat 522  
DB 561 gtgatgtcttccatgtggtgaggaacagatctcgtctgttcaagagatcgtggtggaagaac 620  
QY 523 ta 524  
DB 621 ta 622

RESULT 4  
AAF32057  
ID AAF32057 standard; cDNA; 702 BP.  
XX AAF32057;  
AC  
XX 10-APR-2001 (first entry)  
DT  
DE Arabidopsis eIF-5A coding sequence.  
DE  
KW eIF-5A; eukaryotic initiation factor 5A; senescence inhibition; ss.  
XX Arabidopsis sp.  
OS  
XX  
PN WO200102592-A2.  
XX  
PD 11-JAN-2001.  
XX  
PF 06-JUL-2000; 2000WO-US18364.  
XX  
PR 06-JUL-1999; 99US-0348675.  
PR 19-JUN-2000; 2000US-0597771.  
XX  
PA (SENE-) SENESCO INC.

XX Thompson JE, Wang T, Lu DL;  
XX WPI; 2001-061978/07.  
DR P-PSDB; AAB66879.  
XX Tomato, Arabidopsis and carnation cDNA clones encoding  
PT senescence-induced deoxyhypusine synthase and eif-5a, useful for  
PT inhibiting senescence in a plant when introduced in reverse orientation  
PT into the genome of the plant -  
XX  
XX Claim 5; Fig 15; 135bp; English.  
XX  
XX The present sequence is the coding sequence for Arabidopsis eukaryotic  
CC initiation factor 5A (eif-5A). The eif-5A coding sequence, when  
CC introduced into a plant cell in reverse orientation, inhibits expression  
CC of the endogenous eif-5a gene. The present sequence is useful for  
CC altering age-related senescence and/or environmental stress-related  
CC senescence, for inhibiting seed aging and for increasing seed yield in a  
CC plant. In addition, the inhibition of senescence in a plant results in  
CC increased resistance of the plant to environmental stress-induced and/or  
CC pathogen-induced senescence, increased plant biomass, delayed fruit  
CC softening and spoilage.  
XX  
XX Sequence 702 BP; 186 A; 156 C; 141 G; 219 T; 0 other:

Query Match 38.3%; Score 298.6; DB 22; Length 702;  
Best Local Similarity 77.8%; Pred. No. 1,7e-68;  
Matches 374; Conservative 0; Mismatches 104; Indels 3; Gaps 1;

QY 39 aacgatcgcagacgaacaccatttgatgcacaagcgacatcgtgctcccaaac 98  
DB 52 aacacatgcgcagagagacacacactctgagccca--gtgacgcgagcgctccaaac 108  
QY 99 ttcccacagcaagctggaacacatcgtaagaatggtacatcgttcaaaagcgctcc 158  
DB 109 ctaccctcaacaagctggaacacatcgtaagaatggtacatcgttcaaaatcgctcc 168  
QY 159 ctgcaaggtggtgaggtctcactcaaaaactggaagaacaggaatgctaatagtca 218  
DB 169 ctgcaaggtggtgaggtctcactcaaaaactggaagaacaggaatgctaatagtca 228  
QY 219 cttgtggaatggaatcttcaatggaagaagaactggaagatactgtccgtcccca 278  
DB 229 ttgttagctattgatacttcaccagaactcgaaagataattgttcctctcccca 288  
QY 279 caattgtggtggtccacatgtaacggtacacgactatagctgtatctctgaaga 338  
DB 289 caattgtggtggtccacatgtaacggtacacgactatagctgtatctctgaaga 348  
QY 339 tggttgtgtcactctactgaagaagtgaacaacagaactgactcaggtctccac 398  
DB 349 tggatagtcagttgtgtgactgatacaggtagtaacagaatgacttaagctccctaa 408  
QY 399 cgaatgaaactgtcgaagcaggttaagaatggtgtccagaagaagaagatcttgygt 458  
DB 409 tgaagacactcgtctcccaacagatcaagaatggtgttgaatgaagaagaatcagtggt 468  
QY 459 gtctgtatgtctgcgtgagcggaagagacattaacgcttlaagatgtgtgtaccaa 518  
DB 469 gagtgaatgtcagcatgtgagaggaacagatcaatgctcttaagaactcgtgtccaa 528  
QY 519 g 519  
DB 529 g 529

RESULT 5  
AAC46522  
ID AAC46522 standard; DNA; 868 BP.  
XX  
AC AAC46522;

XX 18-OCT-2000 (first entry)  
DT  
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KW Hybridization assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic;  
KW pathway; promoter; termination sequence; corn; ss.  
XX  
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KW metabolic pathway; promoter; termination sequence; ss.  
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Dd	58 cctcacaaagctggagaccatccgtaagaattggttatcatcgatatcaaaaatcgtccctgc	117
OY	163 aaggttgttgaggtctccaattcaaaactgaaaaacacgacgaatgataatgatactt	222
Dd	118 aaggttgttgaggtctccaattcaaaactgaaaaacgacgaatgataatgatactt	177
OY	223 gggggaattggaattcttcaatggaagaacctggaaagatatcgctccgccccaat	282
Dd	178 gaagcattgatactctcccccagcaagaacctcgaaagatatgcttccctccccaat	237
OY	283 tgtgatgtgccaatgttaacgttaacgatacagtatgatatctctgaagaattg	342
Dd	238 tgtgatgtcccatatgtaacgtaactgtgttatcaagctgattacattctgaagaattga	297
OY	343 ttgtctcaactctctactctaagaatggaacacocaaagatgacctgggttccccacgat	402
Dd	298 tatgtgaatttgttgactgtatacagtlagtaaccaagatgacctgaagccctaatgat	357
OY	403 gaaatctgctgaagcaggtttaagaatggtctccaagaaaggaagatcttgtgtgct	462
Dd	358 gaacctctgtctcaaaagataagatggtggttgatgatgaaagaatcagtygtygat	417
OY	463 gtatgtctgcgattggcggaagaagaataacgcggttaagaatttgtaccag	519
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KM protein identification; signal transduction pathway;		
KW metabolic pathway; promoter; termination sequence; ss.		
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DT 18-OCT-2000 (first entry)

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DB	258	gaggttcttactctcaagacgtgtaagcatgcatgccaatgccaactttgtgcata	317
QY	232	gacatttcaatggaagaacactggaagatatcgttccgtccctcccaacaattgtatgtg	291
DB	318	gacatatccaacggaanaagccttgaagatatgttcttcattcacacaacaattgtatalt	377
QY	292	ccacatgttcaacgttaccgactatcagctgattgatatactctgaagaatggtttgtcca	351
DB	378	ccgcatgtgaacgctacgtacgacacgctgattgatataatcagaagatggaattgtgcagc	437

Oy	352	ccttctaccggaagatggcgaacaaacgaagaagtacttaggccttcaccaacgatgaaaactcg	411
Dd	438	cctctctactcttcagatggccaacaactaaggatgaccttaagactcccaacgtatgagactctc	497
Oy	412	ctgaacgaagttcaataagacgggtctccacgaagaagaagactctgtgtgtcgtcatgtct	471
Dd	498	gttgcccacagatcaagaagaagggtcttgcgaagcgcgaagagatcttgttgcattccagtc	557
Oy	472	ggcagttggggaaggaacaaattaagccgcttaagatgattgtgtaccaaagaatttatgtc	531
Dd	558	gcatactgggggaaggacgaactctgcgcgtcgaagagatgtctgcgcccaagtaacttaactc	617
Oy	532	catggca 538	
Dd	618	cttggaa 624	
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AC	AAC35499 standard; DNA; 761 BP.		
XX	AAC35499;		
DT	17-OCT-2000 (first entry)		
XX			
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 10417.		
DE			
KW	Hybridisation assay; genetic mapping; gene expression control;		
KM	protein identification; signal transduction pathway;		
XX	metabolic pathway; promoter; termination sequence; ss.		
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
PD			
XX	06-SEP-2000.		
PF	25-FEB-2000; 2000EP-0301439.		
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Best Local Similarity 75.3%; Pred. No. 2,9e-65;  
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Qy 99 ttcccaagcgaagctggaaccatccgtaagaatggtttacatcgtttcaaaagcgctcc 158  
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Db 543 ctgcaaggtgtgtgaggttccacattcaaaacttgaaacacgacagatgcttaaatgtca 602  
Qy 219 cttgttgcaattgacatttcaatggaagaacactggaagatgcttcgctcccca 278  
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Qy 279 caattgagatgtgcacacatgtaaacgtaacgcgtacatcatcagctgattgtatctctgaga 338



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Db 663 caattgtaatcttcacatgtaacgcgtgtgtattaccagttcgatcatgatatcaacgagga 722  
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QY 459 gtctgtatgtctgcatagtggcgaagaagacagatlaacgcggttaaggaatgtgtgtaccaa 518  
Db 843 gtctgtacatgtcttcacatgagagagagacagatctgtgcgtaagaagtgtgtgtgtg 902  
QY 519 gaattagttatgt 531  
Db 903 caagtaacaagct 915

RESULT 12  
AAA31536  
ID AAA31536 standard; DNA; 415 BP.  
XX  
XX AAA31536;  
AC  
XX  
DT 05-JUN-2000 (first entry)  
XX  
XX  
DE Plant microsatellite marker #497.  
XX  
KW Plant microsatellite sequence; core repeat sequence; detection; probe;  
KW DNA polymorphism; genome mapping; physical mapping; fingerprinting;  
KW variety identification; genetic variability evaluation; primer; ss.  
XX  
OS Eucalyptus grandis.  
OS  
PN WO9967421-A1.  
XX  
XX  
PD 29-DEC-1999.  
XX  
PF 25-JUN-1999; 99MO-NZ00092.  
XX  
PR 25-JUN-1999; 98US-0105307.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
XX  
PI Havukkala IJ, Bloksberg LN, Glenn M.  
XX  
DR WPI: 2000-116958/10.  
XX  
XX  
PT New plant microsatellite markers and associated flanking species for  
PT the detection of polymorphic genetic markers -  
XX  
XX  
PS Claim 1; Page 223; 392pp; English.  
XX  
XX  
CC Sequences AAA31040-A32093 represent novel plant microsatellite sequences  
CC and associated flanking species. The sequences comprise a central core  
CC repeat sequence, especially selected from the sequences AAA32094-A32096  
CC with left and right flanking sequences. The polynucleotide sequences  
CC can be used in the detection of DNA polymorphisms, in genome mapping,  
CC in physical mapping, in positional cloning of genes, in variety  
CC identification and in evaluation of genetic variability within and  
CC between plant tissues, populations, cultivars, species and species  
CC groups. They may also be used to design hybridization probes for  
CC oligonucleotide fingerprinting and library screening and to design  
CC primers for microsatellite-primed PCR. Microsatellite markers are  
CC useful to locate specific economically useful genes in plant genomes.  
XX  
XX  
SQ Sequence 415 BP; 120 A; 95 C; 104 G; 96 T; 0 other;

Query Match 35.3%; Score 275.2; DB 21; Length 415;

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Matches 330; Conservative 0; Mismatches 73; Indels 1; Gaps 1;  
QY 31 agagagagaagatgtcgcagcaagaacacacatttgaftcaaggcaatgtgtgtcc 90  
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QY 91 tcaaaaactttccacagcaagcttgaacacatccgttaagaatgttacaatcgatcaaa 150  
Db 70 tcccaagcgtlaacccgcagcagccgcacacatccgcaagaatgttacaatcgatcaaa 129  
QY 151 ggcctccctgcgaaggttgttgaagttccacattcaaaaacttgaaaaacagacatgtc 210  
Db 130 gaatgcgccctgcgaaggttgttgaagttccacattcaaaaacttgaaaaacagacatgtc 189  
QY 211 aaatgtcaatttgttgcgaatttgaacatttcaatggaagaagaacttgaagatcgttcg 270  
Db 190 aagtgccacttgcgttggagattgatatctcaatgtggaagaagaacttgaagatcgttc 249  
QY 271 tccctcccaattgtgattgtgcacatgttaaccgttacccgatacagctgattgatac 330  
Db 250 tctgtccacaactgtgattgttccatgattatcattgcacatgatacattgatac 309  
QY 331 tctgaagatgttctgttctcacttcttaactgaagatggaacacacagatgactcagg 390  
Db 310 tctgaagatgttctgttctcacttcttgaactgaagaatggaacacacagatgactcagg 369  
QY 391 ctccaccagatgaanaatctgtgaagcaggttaagaatgtgt 434  
Db 370 -ttccacagatgaacagctgtcttaagcagattaaagatgtgt 412

RESULT 13  
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ID AAC39781 standard; DNA; 777 BP.  
XX  
XX AAC39781;  
AC  
XX  
DT 17-OCT-2000 (first entry)  
XX  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 25879.  
XX  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW Protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
XX  
OS Arabidopsis thaliana.  
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DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65573.

KM Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

OS Arabidopsis thaliana.

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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
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PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161922.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 31.1%; Score 242.8; DB 21; Length 522;  
Best Local Similarity 75.6%; Pred. No. 6.5e-54;  
Matches 301; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

OY 52 gaagaacacatttgtaagtcagatgctggtgctctcaaaacttcccaagcaa 111  
DB 96 gagagacacacttcgaatcgaaagccgacgcgagcgtcccaagacttaccgcagcag 155

OY 112 gctgaaccatccgtaagaatcgtttacatcgttacaagcgctccctgcaagtgtgt 171  
DB 156 gctggcacccgtccgtaagaacggtcttcacgttcatacaagaacgcccctgcaagtgtgt 215  
OY 172 gaggtctccacttcaaaaactggaacaacacgacatgctaattcaacttgttgcaatt 231  
DB 216 gaggttctacctcaagaactgtaagcatgttcacaaatgccacttgttgcacata 275  
OY 232 gacatttccaatgtgaagaactggaagatatacgttccgtctcccaaatgtgattgt 291  
DB 276 gatatattcaacggaagaaagctcgaagatatcgttccctcgtlccacaacactgtgatact 335  
OY 292 ccacatgttaacgctfacccgactatcagctgataatctctcgaagaatgtgttcttca 351  
DB 336 ccgcactgtgaacocgctacgtgagtaicagctgttgatatacagagatgtgttgagc 395  
OY 332 ctcttactgaagaagtgaacaacccaaggaatgaactcgaagcttccacogatgaaatctg 411  
DB 396 ctcttactcagatgagcaaacactaagatgatcttlaagctcccaactgtatgaagactctt 455  
OY 412 ctgaagcaggttaagaatcgtgttccaggaaggaagga 449  
DB 456 gtgcccacagatcaagaagggttgaagaatgtgcaagga 493

Search completed: September 10, 2002, 21:48:04  
Job time: 3296 sec

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